II. IN THE SPECIFICATION

Please amend the specification as follows. In compliance with the proposed 37 C.F.R. § 1.121, deleted language is shown by strikethrough and corrections are shown by underlining.

At page 22, line 3 (U.S. Published Application US 2003/0051266 ("Pub. App.") at ¶ 157), please replace the paragraph starting with "In Tables 1-15 that follow" with the following paragraph:

In Tables 1-15 that follow, the common names of genes are listed, as well as their GeneCards identifiers (Rebhan *et al.*, 1997, GeneCards: encyclopedia for genes, proteins and diseases, Weizmann Institute of Science, Bioinformatics Unit and Genome Center (Rehovot, Israel)~~; http://bioinfo.weizmann.ac.il/cards~~). GenBank accession numbers, UniGene accession numbers, and Mouse Genome Informatics (MGI) Database accession numbers where available are also listed. GenBank is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (Benson *et al.*, 2000, Nucleic Acids Res. 28(1): 15-18 ~~; http://www.ncbi.nlm.nih.gov/Genbank/index.html~~). The GenBank accession number is a unique identifier for a sequence record. An accession number applies to the complete record and is usually a combination of a letter(s) and numbers, such as a single letter followed by five digits (*e.g.*, U12345), or two letters followed by six digits (*e.g.*, AF123456).

At page 22, line 19 (Pub. App. ¶ 159), please replace the paragraph starting with "UniGene" with the following paragraph:

UniGene ~~(http://www.ncbi.nlm.nih.gov/UniGene)~~ is an experimental system for automatically partitioning GenBank sequences into a non-redundant set of gene-oriented clusters for cow, human, mouse, rat, and zebrafish. Within UniGene, expressed sequence tags (ESTs) and full-length mRNA sequences are organized into clusters that each represent a unique known or putative gene. Each UniGene cluster contains related information such as the tissue types in which the gene has been expressed and map location. Sequences are annotated with mapping and expression information and cross-referenced to other resources. Consequently, the collection may be used as a resource for gene discovery.

At page 22, line 27 (Pub. App. ¶ 160), please replace the paragraph starting with "The Mouse Genome Informatics" with the following paragraph:

The Mouse Genome Informatics (MGI) Database is sponsored by the Jackson Laboratory ~~(http://www.informatics.jax.org/mgihome)~~. The MGI Database contains information on mouse genetic markers, mRNA and genomic sequence information, phenotypes, comparative mapping data, experimental mapping data, and graphical displays for genetic, physical, and cytogenetic maps.

At page 80, line 21 (Pub. App. at ¶ 277), please replace the paragraph starting with "Once the transgenic mice are generated" with the following:

Once the transgenic mice are generated they may be bred and maintained using methods well known in the art. By way of example, the mice may be housed in an environmentally controlled facility maintained on a 10 hour dark: 14 hour light cycle or other appropriate light cycle. Mice are mated when they are sexually mature (6 to 8 weeks old). In certain embodiments, the transgenic founders or chimeras are mated to an unmodified animal (*i.e.*, an animal having no cells containing the transgene). In a preferred embodiment, the transgenic founder or chimera is mated to C57BL/6 mice (Jackson Laboratories). In a specific embodiment where the transgene is introduced into ES cells and a chimeric mouse is generated, the chimera is mated to 129/Sv mice, which have the same genotype as the embryonic stem cells. Protocols for successful breeding are known in the art ~~[See hhttp://www.informatics.jax.org/mgihome]~~ (see, *e.g.*, Silver, *Mouse Genetics, Concepts and Applications*, Oxford University Press, 1995). Preferably, a founder male is mated with two females and a founder female is mated with one male. Preferably two females are rotated through a male's cage every 1-2 weeks. Pregnant females are generally housed 1 or 2 per cage. Preferably, pups are ear tagged, genotyped, and weaned at approximately 21 days. Males and females are housed separately. Preferably log sheets are kept for any mated animal, by example and not limitation, information should include pedigree, birth date, sex, ear tag number, source of mother and father, genotype, dates mated and generation.

At page 92, line 7 (Pub. App. at ¶ 334), please replace the paragraph beginning with "The starting point for overgo design is to obtain sequence information" with the following:

The starting point for overgo design is to obtain sequence information for the gene of interest. The software packages required for overgo design require this sequence to

be in FASTA format ~~(http://www.ncbi.nlm.nih.gov/BLAST/fasta.html)~~ (Basic Local Alignment Search Tool ("BLAST") available from National Center for Biotechnology Information ("NCBI")). The sequence used for overgo design should genomic, but cDNA sequences have been used successfully. To design a probe, a region of approximately 500bp is selected. The 500bp region should flank the gene's start codon (ATG) for probe design. This strategy gives a high probability of identifying BACs containing the 5' end of the gene (and presumably many or all of the relevant transcriptional control elements. Selected sequences are screened for the presence of known murine DNA repeat sequences using the Repeat Masker program ~~(http://ftp.genome.washington.edu/cgi-bin/-RepeatMasker)~~ (available from University of Washington, Seattle, WA). Oligonucleotides or "overgos" are then designed using Overgomaker ~~(http://genome.wustl.edu/gsc/overgo/overgo.html)~~ (available from Washington University, St. Louis, MO). The overgo design program scans sequences and identifies two overlapping 24mers that have a balanced GC content, and an overall GC content between 40-60%. Once gene specific overgos have been designed, they are checked for uniqueness by using the BLAST program (NCBI) to compare them to the nr nucleic acid database (NCBI). Overgos that have significant BLAST scores for genes other than the gene of interest, i.e., could hybridize to genes other than the gene of interest, are redesigned.

At page 97, line 29 (Pub. App. at ¶ 457), please replace the paragraph beginning with "The CTIB and RPCI-23 BAC library filters com as sets of 5-10 filters" and continuing to page 99 with the following:

The CTIB and RPCI-23 BAC library filters come as sets of 5-10 filters that have 30-50,000 clones spotted in duplicate on each filter. Following autoradiography, positive clones appear as small dark spots. Because clones are spotted in duplicate, true positives always appear as twin spots within a subdivision of the macroarray. Using templates and positioning aids provided by the filter manufacturer, unique clone identities are obtained for each positive clone. Once the identities of clones for each probe have been identified, they are ordered from BACPAC Resources ~~(http://www.chori.org/bacpac/)~~ (Children's Hospital Oakland Research Institute, Oakland, CA) or Research Genetics ~~(http://www.resgen.com/)~~ (ResGen™, Invitrogen Corp., Carlsbad, CA). To confirm that clones have been correctly identified, each clones is rescreened by PCR using gene specific primers that amplify a portion of the 5' or the 3' end of the gene. In some cases, clones are tested for the presence of both 5' and 3' end amplicons. Other BAC libraries, including those

from non-commercial sources may be used. Clones may be identified using the hybridization method described above to filters with arrayed clones having an identifiable location on the filter so that the corresponding BAC of any positive spots can be obtained.

Please replace the paragraph on page 98, line 26, (Pat. App. at ¶ 462) beginning with "A mouse BAC library, *e.g.*, a RPCI-23 BAC library" with the following:

A mouse BAC library, e.g., a RPCI-23 BAC library, can be fingerprinted using the methods of Soderlund et al. (2000, Genome Res. 10(11):1772-87; incorporated herein by reference in its entirety). BACs are fingerprinted using HindIII digestion digests. Digests are run out on 1% agarose gels, stained with sybr green (Molecular Probes) and then visualized on a Typhoon fluoroimager (Amersham Pharmacia). Gel image data is acquired using the "IMAGE" program (Sanger ~~Center; http://www.sanger.ac.uk/~~ Institute, Hinxton, Cambridge, UK). Data from "IMAGE" is then passed along to the analysis program "FPC" (fingerpring contig)(Sanger ~~Center; http://www.sanger.ac.uk/~~ Institute, Hinxton, Cambridge, UK). Using FPC, the data from a publicly available genome database can be queried to determine if the insert of a particular BAC has been fingerprinted and contigged. BAC fingerprint information has been generated by the University of British Columbia Genome Mapping Project ~~(http://www.begsc.bc.ca/projects/mouse_mapping)~~ (Genome Sciences Center, BC Cancer Agency, Vancouver, BC, Canada) and can be used for assembling BAC contigs. Preferably, contig information from publicly available databases is used to select clones for BAC modification as described above.

Please replace the paragraph beginning with "Using Primer3 program (Massachusetts Institute of Technology" on page 103, line 34 (Pub. App. at ¶ 528) with the following paragraph:

Using Primer3 program ~~(Massachusetts Institute of Technology (http://www genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi)~~ (developed by Massachusetts Institute of Technology, Whitehead Institute, Cambridge, MA and Howard Hughes Medical Institute, Chevy Chase, MD), a AscI site is added in the 5' forward primer and a SmaI site is added in the 3' reverse primer.